



Blast 2 Sequences results

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BLAST

OMIM

Taxonomy

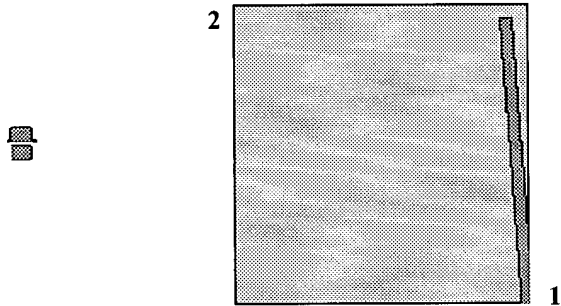
Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.3 [Apr-24-2002]

Match: Mismatch: gap open: gap extension:
 x_dropoff: expect: wordsize: Filter ☒ Align

Sequence 1 [gi_4096271](#) Human MHC Class II HLA DRB1 gene, exon 2, partial cds. **Length** 262 (1 .. 262)

Sequence 2 [lcl|seq_2](#) **Length** 19 (1 .. 19)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 37.2 bits (19), Expect = 8.3
 Identities = 19/19 (100%)
 Strand = Plus / Minus



Query: 244 gtgagagcttcacagtgc 262
 |||||
 Sbjct: 19 gtgagagcttcacagtgc 1

CPU time: 0.05 user secs. 0.05 sys. secs 0.10 total secs.

Lambda K H
 1.33 0.621 1.12

Gapped
 Lambda K H
 1.33 0.621 1.12

Matrix: blastn matrix:1 -2
 Gap Penalties: Existence: 5, Extension: 2
 Number of Hits to DB: 1
 Number of Sequences: 0
 Number of extensions: 1
 Number of successful extensions: 1
 Number of sequences better than 10000.0: 1
 length of query: 262
 length of database: 5,692,721,829
 effective HSP length: 24
 effective length of query: 238

effective length of database: 5,564,683,269
effective search space: 1324394618022
effective search space used: 1324394618022
T: 0
A: 30
X1: 6 (11.5 bits)
X2: 26 (50.0 bits)
S1: 12 (23.8 bits)
S2: 14 (27.6 bits)